

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
KLASS, MICHAEL R.
RUSSELL, JOHN C.
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(ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE LUNG

(iii) NUMBER OF SEQUENCES: 20

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Abbott Laboratories
(B) STREET: 100 Abbott Park Road
(C) CITY: Abbott Park
(D) STATE: IL
(E) COUNTRY: USA
(F) ZIP: 60064-3500

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/048,810
(B) FILING DATE: 05-JUN-1997

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Becker, Cheryl L.
(B) REGISTRATION NUMBER: 35,441
(C) REFERENCE/DOCKET NUMBER: 6104.US.01

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 847/935-1729
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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 200
- (D) OTHER INFORMATION: /note= "N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCCACCGGG	ACTTCAGTGT	CTCCTCCATC	CCAGGAGCGC	AGTGGCCACT	ATGGGGTCTG	60
GGCTGCCCC	TGTCTCCTC	TTGACCCCTC	TTGGCAGCTC	ACATGGAACA	GGGCCGGGTA	120
TGACTTTGCA	ACTGAAGCTG	AAGGAGTCTT	TTCTGACAAA	TTCCTCCTAT	GAGTCCAGCT	180
TCCTGGAATT	GCTTGAAAAN	TCTGCCTCCT	CCTCCATCTC	CCTTCAGGGA	CCAGCGTCA	239

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACCGGGACTT	CAGTGTCTCC	TCCATCCCAG	GAGCGCAGTG	GCCACTATGG	GGTCTGGGCT	60
GCCCCCTTGT	CTCCTCTTGA	CCCTCCTTGG	CAGCTCACAT	GGAACAGGGC	CGGGTATGAC	120
TTTGCAACTG	AAGCTGAAGG	AGTCTTTCT	GACAAATTCC	TCCTATGAGT	CCAGCTTCCT	180
GGAATTGCTT	AAAAAGTCTG	CCTCCTCCTC	CATCTCCCTT	CAGGGACCA		229

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAGGAGCGCA	GTTGGCCACTA	TGGGGTCTGG	GCTGCCCTT	GTCCTCCTCT	TGACCCCTCCT	60
TGGCAGCTCA	CATGGAACAG	GGCCGGGTAT	GACTTGCAA	CTGAAGCTGA	AGGAGTCTTT	120
TCTGACAAGT	TCCTCCTATG	AGTCCAGCTT	CCTGGAATTG	CTTGAAAAGC	TCTGCCTCCT	180

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 68
- (D) OTHER INFORMATION: /note= "N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:
(A) NAME/KEY: base_polymorphism
(B) LOCATION: 101
(D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:
(A) NAME/KEY: base_polymorphism
(B) LOCATION: 124
(D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:
(A) NAME/KEY: base_polymorphism
(B) LOCATION: 131
(D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCAACACCAT	GTTGTCTGCA	ACACATGACA	GCCATTGAAG	CCTGTGTCT	TCTTGGCCCG	60
GGCTTTNGG	CGGGGAATGC	AGGAGGCAGG	CCCCGACCCT	NTCTTCAGC	AGGCCCCCAC	120
CCTNCTGAGT	NGCAATAAAT	AAAATTCGGT	ATGCTGAATT	CAATA		165

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 389 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CAGGAGCGCA	GTGGCCACTA	TGGGGTCTGG	GCTGCCCTT	GTCCTCCTCT	TGACCCTCCT	60
TGGCAGCTCA	CATGGAACAG	GGCCGGGTAT	GACTTGC	CTGAAGCTGA	AGGAGTCTTT	120
TCTGACAAGT	TCCTCTATG	AGTCAGCTT	CCTGGAATTG	CTTGAAAAGC	TCTGCCCTCT	180
CCTCCATCTC	CCTTCAGGGA	CGACGTCAC	CCTCCACCAT	GCAAGATCTC	AACACCATGT	240
TGTCTGCAAC	ACATGACAGC	CATTGAAGCC	TGTGTCTTC	TTGGCCCGGG	CTTTTGGGCC	300
GGGGATGCAAG	GAGGCAGGCC	CCGACCCCTGT	CTTTCAGCAG	GCCCCCACCC	TCCTGAGTGG	360
CAATAAATAA	AATTCCGGT	T	GCTGAATT			389

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 413 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACCGGGACTT	CAGTGTCTCC	TCCATCCCAG	GAGGCAGTG	GCCACTATGG	GGTCTGGGCT	60
GCCCCCTTGT	CTCCTCTTGA	CCCTCCTTGG	CAGCTCACAT	GGAACAGGGC	CGGGTATGAC	120
TTTGCAACTG	AAGCTGAAGG	AGTCTTTCT	GACAAATTCC	TCCTATGAGT	CCAGCTTCCT	180
GGAAATTGCTT	AAAAAGCTCT	GCCTCCTCCT	CCATCTCCCT	TCAGGGACCA	GCGTCACCCT	240
CCACCATGCA	AGATCTAAC	ACCATGTTGT	CTGCAACACA	TGACAGCCAT	TGAAGCCTGT	300
GTCCTTCTTG	GCCCCGGGCTT	TTGGGCCGGG	GATGCAGGAG	GCAGGCCCG	ACCCGTGTCTT	360
TCAGCAGGCC	CCCACCTCC	TGAGTGGCAA	TAAATAAAAT	TCGGTATGCT	TGA	413

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCCACCGGG	ACTTCAGTGT	CTCCTCCATC	CCAGGAGCGC	AGTGGCCACT	ATGGGGTCTG	60
GGCTGCCCT	TGTCCCTCTC	TTGACCCCTCC	TTGGCAGCTC	ACATGGAACA	GGGCCGGGTA	120
TGACTTTGCA	ACTGAAGCTG	AAGGAGTCTT	TTCTGACAAA	TTCCTCCTAT	GAGTCCAGCT	180
TCCTGGAATT	GCTTGAAAG	CTCTGCCTCC	TCCTCCATCT	CCCTTCAGGG	ACCAGCGTCA	240
CCCTCCACCA	TGCAAGATCT	CAACACCATG	TTGTCTGCAA	CACATGACAG	CCATTGAAGC	300
CTGTTGCTCT	CTTGGCCCGG	CGTTTGGGC	CGGGGATGCA	GGAGGCAGGC	CCCGACCCCTG	360
TCTTCAGCA	GGCCCCCACC	CTCCTGAGTG	GCAATAAATA	AAATTCGGTA	TGCTGAATT	420
AATA						424

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGCTCGGAAT	TCCGAGCTTG	GATCCTCTAG	AGCGGCCGCC	GACTAGTGAG	CTCGTCGACC	60
CGGGAATT						68

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AATTAATTCC	CGGGTCGACG	AGCTCACTAG	TCGGCGGCCG	CTCTAGAGGA	TCCAAGCTCG	60
GAATTCCG						68

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTTTTTTTTT	TTTTTTTTTT	TTTTTC				26
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(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGTAAAACGA CGGCCAGT

18

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AAGGACACAG GCTTCAATGG

20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCCGCCATGG ACCTGCTGCT GGACTCTTAT AG

32

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGGCCGCC ACAATGATGT CATAGACACG

30

(2) INFORMATION FOR SEO ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

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Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr Leu Leu Gly Ser
      1          5          10          15
Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu Lys Leu Lys Glu
      20          25          30
Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe Leu Glu Leu Leu
      35          40          45
Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly Thr Ser Val Thr
      50          55          60
Leu His His Ala Arg Ser Gln His His Val Val Cys Asn Thr
      65          70          75

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(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser	Ser	His	Gly	Thr	Gly	Pro	Gly	Met	Thr	Leu	Gln	Leu	Lys	Leu	Lys
1				5					10				15		
Glu	Ser	Phe	Leu	Thr	Asn	Ser	Ser	Tyr	Glu	Ser	Ser	Phe			
			20					25							

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Glu	Lys	Leu	Cys	Leu	Leu	Leu	His	Leu	Pro	Ser	Gly	Thr	Ser	Val	Thr
1				5				10				15			
Leu	His	His	Ala	Arg	Ser	Gln	His	His	Val	Val	Cys	Asn	Thr		
			20					25				30			

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Glu	Lys	Ser	Ala	Ser	Ser	Ser	Ile	Ser	Leu	Gln	Gly	Pro	Ala	Ser	Pro
1				5				10				15			
Ser	Thr	Met	Gln	Asp	Leu	Asn	Thr	Met	Leu	Ser	Ala	Thr	His	Asp	Ser
			20					25				30			
His															

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His Thr Glu His
1 5 10 15
His His His His His
20

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100